

SEQUENCE LISTING

<110> Ellsworth, Jeff L.

<120> METHODS FOR ADMINISTERING FGF18

<130> 02-21

<150> 60/416,670

<151> 2002-10-07

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 917

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(621)

<400> 1

atg tat tca gcg ccc tcc gcc tgc act tgc ctg tgt tta cac ttc ctg	48
Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu	
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ctg ctg tgc ttc cag gta cag gtg ctg gtt gcc gag gag aac gtg gac	96
Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp	
20 25 30	
ttc cgc atc cac gtg gag aac cag acg cgg gct cgg gac gat gtg agc	144
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser	
35 40 45	
cgt aag cag ctg cgg ctg tac cag ctc tac agc cgg acc agt ggg aaa	192
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys	
50 55 60	
cac atc cag gtc ctg ggc cgc agg atc agt gcc cgc ggc gag gat ggg	240
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly	
65 70 75 80	
gac aag tat gcc cag ctc cta gtg gag aca gac acc ttc ggt agt caa	288
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln	
85 90 95	
gtc cgg atc aag ggc aag gag acg gaa ttc tac ctg tgc atg aac cgc	336
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg	
100 105 110	
aaa ggc aag ctc gtg ggg aag ccc gat ggc acc agc aag gag tgt gtg	384
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val	
115 120 125	
ttc atc gag aag gtt ctg gag aac aac tac acg gcc ctg atg tcg gct	432
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala	
130 135 140	

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aag tac tcc ggc tgg tac gtg ggc ttc acc aag aag ggg cgg ccg cgg 480
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145          150          155          160

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aag ggc ccc aag acc cgg gag aac cag cag gac gtg cat ttc atg aag 528
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
          165          170          175

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cgc tac ccc aag ggg cag ccg gag ctt cag aag ccc ttc aag tac acg 576
Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
          180          185          190

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acg gtg acc aag agg tcc cgt cgg atc cgg ccc aca cac cct gcc 621
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
          195          200          205

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taggccaccc cgccgcgggcc ctcaggtcgc cctggccaca ctcacactcc cagaaaactg 681
catcagagga atatttttac atgaaaaata aggattttat tgttgacttg aaacccccga 741
tgacaaaaga ctcacgcaaa gggactgtag tcaaccacaca ggtgcttgtc tctctctagg 801
aacagacaac tctaaactcg tccccagagg aggacttgaa tgaggaaacc aacactttga 861
gaaaccaaag tcctttttcc caaaggttct gaaaaaaaaa aaaaaaaaaa ctcgag 917

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<210> 2

<211> 207

<212> PRT

<213> Homo sapiens

<400> 2

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Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
1      5      10
Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp
20     25     30
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
35     40     45
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
50     55     60
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65     70     75     80
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
85     90     95
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
100    105    110
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
115    120    125
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
130    135    140
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145    150    155    160
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
165    170    175
Arg Tyr Pro Lys Gly Gln Pro Glu Leu Gln Lys Pro Phe Lys Tyr Thr
180    185    190
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Ala
195    200    205

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<210> 3

<211> 1023

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(624)

<400> 3

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atg tat tca gcg ccc tcc gcc tgc act tgc ctg tgt tta cac ttt cta 48
Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
1 5 10 15

ctg ctg tgc ttc cag gtt cag gtg ttg gca gcc gag gag aat gtg gac 96
Leu Leu Cys Phe Gln Val Gln Val Leu Ala Ala Glu Glu Asn Val Asp
20 25 30

ttc cgc atc cac gtg gag aac cag acg cgg gct cga gat gat gtg agt 144
Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
35 40 45

cgg aag cag ctg cgc ttg tac cag ctc tat agc agg acc agt ggg aag 192
Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
50 55 60

cac att caa gtc ctg ggc cgt agg atc agt gcc cgt ggc gag gac ggg 240
His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65 70 75 80

gac aag tat gcc cag ctc cta gtg gag aca gat acc ttc ggg agt caa 288
Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
85 90 95

gtc cgg atc aag ggc aag gag aca gaa ttc tac ctg tgt atg aac cga 336
Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
100 105 110

aaa ggc aag ctc gtg ggg aag cct gat ggt act agc aag gag tgc gtg 384
Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
115 120 125

ttc att gag aag gtt ctg gaa aac aac tac acg gcc ctg atg tct gcc 432
Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
130 135 140

aag tac tct ggt tgg tat gtg ggc ttc acc aag aag ggg cgg cct cgc 480
Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
145 150 155 160

aag ggt ccc aag acc cgc gag aac cag caa gat gta cac ttc atg aag 528
Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
165 170 175

cgt tac ccc aag gga cag gcc gag ctg cag aag ccc ttc aaa tac acc 576
Arg Tyr Pro Lys Gly Gln Ala Glu Leu Gln Lys Pro Phe Lys Tyr Thr
180 185 190

aca gtc acc aag cga tcc cgg cgg atc cgc ccc act cac ccc ggc tag 624
Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Gly *
195 200 205

gtccggccac actcaccccc ccagagaact acatcagagg aatatatttta catgaaaaat 684
aaggaagaat ctctattttt gtacattgtg tttaaaagaa gacaaaaact gaacctaaag 744
tcttgggagg agggggcgata ggattccact gttgacctga accccatgac aaaggactca 804
cacaagggga ccgctgtcaa ccacaggtg cttgcctctc tctaggaggt gacaattcaa 864
aactcatccc cagaggagga cttgaacgag gaaactgcga gaaaccaaag tcctttcccc 924
ccaaaggttc tgaaagcaaa caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 984
aaaaaaaaaa aaaaaaaaaa gggcggccgc tctagagga 1023

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<210> 4
 <211> 207
 <212> PRT
 <213> Mus musculus

<400> 4
 Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
 1 5 10 15
 Leu Leu Cys Phe Gln Val Gln Val Leu Ala Ala Glu Glu Asn Val Asp
 20 25 30
 Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
 35 40 45
 Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
 50 55 60
 His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
 65 70 75 80
 Asp Lys Tyr Ala Gln Leu Leu Val Glu Thr Asp Thr Phe Gly Ser Gln
 85 90 95
 Val Arg Ile Lys Gly Lys Glu Thr Glu Phe Tyr Leu Cys Met Asn Arg
 100 105 110
 Lys Gly Lys Leu Val Gly Lys Pro Asp Gly Thr Ser Lys Glu Cys Val
 115 120 125
 Phe Ile Glu Lys Val Leu Glu Asn Asn Tyr Thr Ala Leu Met Ser Ala
 130 135 140
 Lys Tyr Ser Gly Trp Tyr Val Gly Phe Thr Lys Lys Gly Arg Pro Arg
 145 150 155 160
 Lys Gly Pro Lys Thr Arg Glu Asn Gln Gln Asp Val His Phe Met Lys
 165 170 175
 Arg Tyr Pro Lys Gly Gln Ala Glu Leu Gln Lys Pro Phe Lys Tyr Thr
 180 185 190
 Thr Val Thr Lys Arg Ser Arg Arg Ile Arg Pro Thr His Pro Gly
 195 200 205